Amended Claims without Markings

Although a version of "clean" claims are no longer necessary, Applicants are providing this version of the claims as a courtesy to the Examiner.

E1 1 ~~37~~. (Amended) A transgenic plant comprising a recombinant polynucleotide encoding SEQ ID NO: 18, and said transgenic plant has enhanced tolerance to fungal disease due to expression of SEQ ID NO: 18.

39. (Reiterated) The transgenic plant of claim 37, wherein the recombinant polynucleotide comprises SEQ ID NO: 17.

40. (Reiterated) The transgenic plant of claim 37, wherein the recombinant polynucleotide further comprises one or more regulatory sequences.

41. (Reiterated) The transgenic plant of claim 40, wherein said one or more regulatory sequences are selected from the group consisting of a promoter, a transcription initiation start site, an RNA processing signal, a transcription termination site, and a polyadenylation signal.

42. (Reiterated) The transgenic plant of claim 41, wherein said promoter is constitutive, inducible, or tissue-specific.

E2 6 ~~44~~. (Amended) The transgenic plant of claim 1 ~~37~~, wherein said fungal disease is caused by *Fusarium*, *Erysiphe*, *Sclerotinia* or *Botrytis*.

7 ~~45~~. (Amended) A method for enhancing the disease tolerance or resistance of a plant comprising transforming a plant with a recombinant polynucleotide encoding SEQ ID NO: 18, and said transgenic plant has enhanced tolerance to fungal disease due to expression of SEQ ID NO: 18.

47. (Reiterated) The method of claim 45, wherein the recombinant polynucleotide comprises SEQ ID NO: 17.

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48. (Reiterated) The method of claim 45, wherein the recombinant polynucleotide further comprises one or more regulatory sequences.

49. (Reiterated) The method of claim 48, wherein said one or more regulatory sequences are selected from the group consisting of a promoter, a transcription initiation start site, an RNA processing signal, a transcription termination site, and a polyadenylation signal.

50. (Reiterated) The method of claim 49, wherein said promoter is constitutive, inducible, or tissue-specific.

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12 ~~52.~~ (Amended) The transgenic plant of claim 7 ~~45~~, wherein said fungal disease is caused by *Fusarium, Erysiphe, Sclerotinia* or *Botrytis*.

13 ~~53.~~ (Amended) A method for altering the expression levels of at least one gene in a plant comprising transforming the plant with a recombinant polynucleotide encoding SEQ ID NO: 18, and said transgenic plant has enhanced tolerance to fungal disease due to expression of SEQ ID NO: 18.

55. (Reiterated) The method of claim 53, wherein the recombinant polynucleotide comprises SEQ ID NO: 17.

56. (Reiterated) The method of claim 53, wherein the recombinant polynucleotide further comprises one or more regulatory sequences.

57. (Reiterated) The method of claim 56, wherein said one or more regulatory sequences are selected from the group consisting of a promoter, a transcription initiation start site, an RNA processing signal, a transcription termination site, and a polyadenylation signal.

58. (Reiterated) The method of claim 57, wherein said promoter is constitutive, inducible, or tissue-specific.

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18 ~~60.~~ (Amended) The transgenic plant of claim 13 ~~53~~, wherein said fungal disease is caused by *Fusarium, Erysiphe, Sclerotinia or Botrytis*.

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61. (Amended) A transgenic plant comprising a recombinant polynucleotide comprising a nucleotide sequence encoding a transcription factor having a conserved domain of a plant AP2 transcription factor, wherein:

said nucleotide sequence encoding said transcription factor hybridizes under high stringency conditions to a polynucleotide sequence encoding an amino acid sequence of residues 145-213 of SEQ ID NO: 18, wherein:

said high stringency conditions comprise 0.2 x SSC and 0.1% SDS at 65° C, and wherein:

said transgenic plant is characterized by enhanced tolerance to fungal disease due to expression of said transcription factor.

62. (Reiterated) The transgenic plant of claim 61, wherein the polynucleotide sequence comprises SEQ ID NO: 17.

63. (Reiterated) The transgenic plant of claim 61, wherein the recombinant polynucleotide further comprises one or more regulatory sequences.

64. (Reiterated) The transgenic plant of claim 63, wherein said one or more regulatory sequences are selected from the group consisting of a promoter, a transcription initiation start site, an RNA processing signal, a transcription termination site, and a polyadenylation signal.

65. (Reiterated) The transgenic plant of claim 64, wherein said promoter is constitutive, inducible, or tissue-specific.

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67. (Amended) The transgenic plant of claim 61, wherein said fungal disease is caused by *Fusarium, Erysiphe, Sclerotinia or Botrytis.*

68. (Amended) A method for enhancing the disease tolerance or resistance in a plant comprising transforming said plant with a recombinant polynucleotide comprising a nucleotide sequence encoding a transcription factor having a conserved domain of a plant AP2 transcription factor, wherein:

said nucleotide sequence encoding said transcription factor hybridizes under high stringency conditions to a polynucleotide sequence encoding a conserved domain comprising an amino acid sequence of residues 145-213 of SEQ ID NO: 18, wherein:

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said high stringency conditions comprise 0.2 x SSC and 0.1% SDS at 65° C, and wherein:

said transgenic plant is characterized by enhanced tolerance to fungal disease due to expression of said transcription factor.

69. (Reiterated) The method of claim 68, wherein the polynucleotide sequence comprises SEQ ID NO: 17.

70. (Reiterated) The method of claim 68, wherein the recombinant polynucleotide further comprises one or more regulatory sequences.

71. (Reiterated) The method of claim 70, wherein said one or more regulatory sequences are selected from the group consisting of a promoter, a transcription initiation start site, an RNA processing signal, a transcription termination site, and a polyadenylation signal.

72. (Reiterated) The method of claim 71, wherein said promoter is constitutive, inducible, or tissue-specific.

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74. (Amended) The transgenic plant of claim 68, wherein said fungal disease is caused by *Fusarium, Erysiphe, Sclerotinia or Botrytis.*

75. (Amended) A transgenic plant comprising a recombinant polynucleotide encoding SEQ ID NO: 18, or the same sequence with one or more conservative substitutions, deletions, or insertions, wherein said transgenic plant has enhanced tolerance to fungal disease due to expression of said SEQ ID NO: 18.

76. (Reiterated) The transgenic plant of claim 75, wherein said fungal disease is caused by *Fusarium, Erysiphe, Sclerotinia or Botrytis.*